



PCT10

RAW SEQUENCE LISTING

DATE: 12/11/2002 P-6

PATENT APPLICATION: US/10/070,240A

TIME: 09:34:59

Input Set : N:\CrF4\11252002\J070240.raw

Output Set: N:\CRF4\12112002\J070240A.raw

1 <110> APPLICANT: WATANABE, TAKUYA
 2 TERA0, YASUKO
 3 SHINTANI, YASUSHI
 4 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR PROTEIN AND DNA
 5 THEREOF
 6 <130> FILE REFERENCE: (46342) 57127
 7 <140> CURRENT APPLICATION NUMBER: US/10/070,240A
 8 <141> CURRENT FILING DATE: 2002-02-27
 9 <150> PRIOR APPLICATION NUMBER: JP 2000-217474
 10 <151> PRIOR FILING DATE: 2000-07-18
 11 <150> PRIOR APPLICATION NUMBER: JO 11-241531
 12 <151> PRIOR FILING DATE: 1999-08-27
 13 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05685
 14 <151> PRIOR FILING DATE: 1999-08-27
 15 <160> NUMBER OF SEQ ID NOS: 34
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 393
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
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 26 20 25 30
 27 Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
 28 35 40 45
 29 Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
 30 50 55 60
 31 Ile Gly Met Ala Leu Val Gly Ile Met Leu Val Cys Gly Ile Gly Asn
 32 65 70 75 80
 33 Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu
 34 85 90 95
 35 Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
 36 100 105 110
 37 Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
 38 115 120 125
 39 Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
 40 130 135 140
 41 Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile
 42 145 150 155 160
 43 Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
 44 165 170 175

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47   Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
48               195               200               205
49   Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
50               210               215               220
51   Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
52   225               230               235               240
53   Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
54               245               250               255
55   Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
56               260               265               270
57   Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
58               275               280               285
59   Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
60               290               295               300
61   Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
62   305               310               315               320
63   Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
64               325               330               335
65   Ile Asn Thr Leu Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr
66   340               345               350
67   Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
68   355               360               365
69   Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
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72   385               390
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85   acc agc ttc ctt tct gtg ctc aac cct cat gga gcc cat gcc act tcc      96
86   Thr Ser Phe Leu Ser Val Leu Asn Pro His Gly Ala His Ala Thr Ser
87               20               25               30
88   ttc cca ttc aac ttc agc tac agc gac tat gat atg cct ttg gat gaa     144
89   Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
90               35               40               45
91   gat gag gat gtg acc aat tcc agg acg ttc ttt gct gcc aag att gtc     192
92   Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val
93       50               55               60
94   att ggg atg gcc ctg gtg ggc atc atg ctg gtc tgc ggc att gga aac     240

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97	ttc atc ttt atc gct gcc ctg gtc cgc tac aag aaa ctg cgc aac ctc	288
98	Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu	
99	85 90 95	
100	acc aac ctg ctc atc gcc aac ctg gcc atc tct gac ttc ctg gtg gcc	336
101	Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala	
102	100 105 110	
103	att gtc tgc tgc ccc ttt gag atg gac tac tat gtg gtg cgc cag ctc	384
104	Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu	
105	115 120 125	
106	tcc tgg gag cac ggc cac gtc ctg tgc acc tct gtc aac tac ctg cgc	432
107	Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg	
108	130 135 140	
109	act gtc tct ctc tat gtc tcc acc aat gcc ctg ctg gcc atc gcc att	480
110	Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile	
111	145 150 155 160	
112	gac agg tat ctg gct att gtc cat ccg ctg aga cca cgg atg aag tgc	528
113	Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys	
114	165 170 175	
115	caa aca gcc act ggc ctg att gcc ttg gtg tgg acg gtg tcc atc ctg	576
116	Gln Thr Ala Thr Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu	
117	180 185 190	
118	atc gcc atc cct tcc gcc tac ttc acc acc gag acg gtc ctc gtc att	624
119	Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile	
120	195 200 205	
121	gtc aag agc cag gaa aag atc ttc tgc ggc cag atc tgg cct gtg gac	672
122	Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp	
123	210 215 220	
124	cag cag ctc tac tac aag tcc tac ttc ctc ttt atc ttt ggc ata gaa	720
125	Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu	
126	225 230 235 240	
127	ttc gtg ggc ccc gtg gtc acc atg acc ctg tgc tat gcc agg atc tcc	768
128	Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser	
129	245 250 255	
130	cgg gag ctc tgg ttc aag gcg gtc cct gga ttc cag aca gag cag atc	816
131	Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile	
132	260 265 270	
133	cgc aag agg ctg cgc tgc cgc agg aag acg gtc ctg gtg ctc atg tgc	864
134	Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys	
135	275 280 285	
136	atc ctc acc gcc tac gtg cta tgc tgg gcg ccc ttc tac ggc ttc acc	912
137	Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr	
138	290 295 300	
139	atc gtg cgc gac ttc ttc ccc acc gtg ttc gtg aag gag aag cac tac	960
140	Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr	
141	305 310 315 320	
142	ctc act gcc ttc tac atc gtc gag tgc atc gcc atg agc aac agc atg	1008
143	Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met	

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144          325          330          335
145      atc aac act ctg tgc ttc gtg acc gtc aag aac gac acc gtc aag tac 1056
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147          340          345          350
148      ttc aaa aag atc atg ttg ctc cac tgg aag gct tct tac aat ggc ggt 1104
149      Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
150          355          360          365
151      aag tcc agt gca gac ctg gac ctc aag aca att ggg atg cct gcc acc 1152
152      Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
153          370          375          380
154      gaa gag gtg gac tgc atc aga cta aaa 1179
155      Glu Glu Val Asp Cys Ile Arg Leu Lys
156      385          390
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159 <211> LENGTH: 1179
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
162 <220> FEATURE:
163 <221> NAME/KEY: CDS
164 <222> LOCATION: (1)..(1179)
165 <400> SEQUENCE: 3
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169      acc agc ttc ctt tct gtg ctc aac cct cat gga gcc cat gcc act tcc 96
170      Thr Ser Phe Leu Ser Val Leu Asn Pro His Gly Ala His Ala Thr Ser
171          20          25          30
172      ttc cca ttc aac ttc agc tac agc gac tat gat atg cct ttg gat gaa 144
173      Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu
174          35          40          45
175      gat gag gat gtg acc aat tcc agg acg ttc ttt gct gcc aag att gtc 192
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177          50          55          60
178      att ggg atg gcc ctg gtg ggc atc atg ctg gtc tgc ggc att gga aac 240
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181      ttc atc ttt atc gct gcc ctg gtc cgc tac aag aaa ctg cgc aac ctc 288
182      Phe Ile Phe Ile Ala Ala Leu Val Arg Tyr Lys Lys Leu Arg Asn Leu
183          85          90          95
184      acc aac ctg ctc atc gcc aac ctg gcc atc tct gac ttc ctg gtg gcc 336
185      Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala
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187      att gtc tgc tgc ccc ttt gag atg gac tac tat gtg gtg cgc cag ctc 384
188      Ile Val Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu
189          115          120          125
190      tcc tgg gag cac ggc cac gtc ctg tgc acc tct gtc aac tac ctg cgc 432
191      Ser Trp Glu His Gly His Val Leu Cys Thr Ser Val Asn Tyr Leu Arg
192          130          135          140
193      act gtc tct ctc tat gtc tcc acc aat gcc ctg ctg gcc atc gcc att 480

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Input Set : N:\Crf4\11252002\J070240.raw

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194   Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile
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197   Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Pro Arg Met Lys Cys
198                               165                               170                               175
199   caa aca gcc act ggc ctg att gcc ttg gtg tgg acg gtg tcc atc ctg      576
200   Gln Thr Ala Thr Gly Leu Ile Ala Leu Val Trp Thr Val Ser Ile Leu
201                               180                               185                               190
202   atc gcc atc cct tcc gcc tac ttc acc acc gag acg gtc ctc gtc att      624
203   Ile Ala Ile Pro Ser Ala Tyr Phe Thr Thr Glu Thr Val Leu Val Ile
204                               195                               200                               205
205   gtc aag agc cag gaa aag atc ttc tgc ggc cag atc tgg cct gtg gac      672
206   Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp Pro Val Asp
207   210                               215                               220
208   cag cag ctc tac tac aag tcc tac ttc ctc ttt atc ttt ggc ata gaa      720
209   Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe Gly Ile Glu
210   225                               230                               235                               240
211   ttc gtg ggc ccc gtg gtc acc atg acc ctg tgc tat gcc agg atc tcc      768
212   Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala Arg Ile Ser
213   245                               250                               255
214   cgg gag ctc tgg ttc aag gcg gtc cct gga ttc cag aca gag cag atc      816
215   Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr Glu Gln Ile
216   260                               265                               270
217   cgc aag agg ctg cgc tgc cgc agg aag acg gtc ctg gtg ctc atg tgc      864
218   Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val Leu Met Cys
219   275                               280                               285
220   atc ctc acc gcc tac gtg cta tgc tgg gcg ccc ttc tac ggc ttc acc      912
221   Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr
222   290                               295                               300
223   atc gtg cgc gac ttc ttc ccc acc gtg ttt gtg aag gag aag cac tac      960
224   Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr
225   305                               310                               315                               320
226   ctc act gcc ttc tac atc gtc gag tgc atc gcc atg agc aac agc atg      1008
227   Leu Thr Ala Phe Tyr Ile Val Glu Cys Ile Ala Met Ser Asn Ser Met
228   325                               330                               335
229   atc aac act ctg tgc ttc gtg acc gtc aag aac gac acc gtc aag tac      1056
230   Ile Asn Thr Leu Cys Phe Val Thr Val Lys Asn Asp Thr Val Lys Tyr
231   340                               345                               350
232   ttc aaa aag atc atg ttg ctc cac tgg aag gct tct tac aat ggc ggt      1104
233   Phe Lys Lys Ile Met Leu Leu His Trp Lys Ala Ser Tyr Asn Gly Gly
234   355                               360                               365
235   aag tcc agt gca gac ctg gac ctc aag aca att ggg atg cct gcc acc      1152
236   Lys Ser Ser Ala Asp Leu Asp Leu Lys Thr Ile Gly Met Pro Ala Thr
237   370                               375                               380
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239   Glu Glu Val Asp Cys Ile Arg Leu Lys
240   385                               390
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 31

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/11/2002
PATENT APPLICATION: US/10/070,240A TIME: 09:35:00

Input Set : N:\Crf4\11252002\J070240.raw
Output Set: N:\CRF4\12112002\J070240A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 7,13
Seq#:31; Xaa Pos. 7

VERIFICATION SUMMARY

DATE: 12/11/2002

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TIME: 09:35:00

Input Set : N:\Crf4\11252002\J070240.raw

Output Set: N:\CRF4\12112002\J070240A.raw

L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0